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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/829,936B

DATE: 06/04/2003

TIME: 15:49:40

Input Set : A:\ep.txt

Output Set: N:\CRF4\06042003\I829936B.raw

3 <110> APPLICANT: Conseiller, Emmanuel
 4 Debussche, Laurent
 5 Gallagher, William
 7 <120> TITLE OF INVENTION: Polypeptide (MBP1) Capable Of Interacting With Oncogenic
 Mutants Of The
 8 P53 Protein
 10 <130> FILE REFERENCE: ST98033
 12 <140> CURRENT APPLICATION NUMBER: 09/829,936B
 13 <141> CURRENT FILING DATE: 2001-04-11
 15 <150> PRIOR APPLICATION NUMBER: FR9812754
 16 <151> PRIOR FILING DATE: 1998-10-12
 18 <160> NUMBER OF SEQ ID NOS: 33
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 23
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Oligonucleotide 5'-1(p53)
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 31 agatctgtat ggaggagccg cag 23
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 29
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence
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 40 <223> OTHER INFORMATION: Oligonucleotide 3' -393 (p53)
 42 <400> SEQUENCE: 2
 43 agatctcatc agtctgagtc aggcccttc 29
 46 <210> SEQ ID NO: 3
 47 <211> LENGTH: 15
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
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 55 ggggcagtgc ctcac 15
 58 <210> SEQ ID NO: 4
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 60 <212> TYPE: DNA
 61 <213> ORGANISM: Artificial Sequence
 63 <220> FEATURE:
 64 <223> OTHER INFORMATION: Oligonucleotide W248 3'
 66 <400> SEQUENCE: 4

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67	gggcctccag ttcat	15
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80	acaaaacatgc acctc	15
83	<210> SEQ ID NO: 6	
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85	<212> TYPE: DNA	
86	<213> ORGANISM: Artificial Sequence	
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89	<223> OTHER INFORMATION: Oligonucleotide G281 3'	
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92	gcgccggcct ctccc	15
95	<210> SEQ ID NO: 7	
96	<211> LENGTH: 23	
97	<212> TYPE: DNA	
98	<213> ORGANISM: Artificial Sequence	
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101	<223> OTHER INFORMATION: Oligonucleotide 5'-73	
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104	agatctgtgt ggcccttgca cca	23
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115	<220> FEATURE:	
116	<221> NAME/KEY: CDS	
117	<222> LOCATION: (1)..(885)	
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121	Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp	
122	1 5 10 15	
124	ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg	96
125	Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu	
126	20 25 30	
128	ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct	144
129	Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro	
130	35 40 45	
132	aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca	192
133	Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro	
134	50 55 60	
136	tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt	240
137	Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys	

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138	65	70	75	80	
140	aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc				288
141	Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile				
142	85	90	95		
144	gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac				336
145	Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn				
146	100	105	110		
148	gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg				384
149	Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu				
150	115	120	125		
152	gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac				432
153	Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His				
154	130	135	140		
156	caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc				480
157	Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg				
158	145	150	155	160	
160	tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac				528
161	Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp				
162	165	170	175		
164	aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct				576
165	Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro				
166	180	185	190		
168	tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg				624
169	Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val				
170	195	200	205		
172	cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc				672
173	Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala				
174	210	215	220		
176	tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac				720
177	Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr				
178	225	230	235	240	
180	att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca				768
181	Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro				
182	245	250	255		
184	gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg				816
185	Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met				
186	260	265	270		
188	aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc				864
189	Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val				
190	275	280	285		
192	ttt gtg gga gcc tat acc ttc tgaagaccct caggagaaggg ccatgtgggg				915
193	Phe Val Gly Ala Tyr Thr Phe				
194	290	295			
196	cccccttccc cctccatag cttaagcagc cccgggggcc tagggatgac cgttctgctt				975
198	aaaggaacta tgatgtaaag gacaataaag ggagaaagaa ggaaaa				1021
201	<210> SEQ ID NO: 9				
202	<211> LENGTH: 295				
203	<212> TYPE: PRT				
204	<213> ORGANISM: Artificial Sequence				

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206 <220> FEATURE:
207 <223> OTHER INFORMATION: Murine MBP1 C-term fragment
209 <400> SEQUENCE: 9
211 Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
212 1 5 10 15
215 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
216 20 25 30
219 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
220 35 40 45
223 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
224 50 55 60
227 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
228 65 70 75 80
231 Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
232 85 90 95
235 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
236 100 105 110
239 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
240 115 120 125
243 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
244 130 135 140
247 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
248 145 150 155 160
251 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
252 165 170 175
255 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
256 180 185 190
259 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
260 195 200 205
263 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
264 210 215 220
267 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
268 225 230 235 240
271 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
272 245 250 255
275 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
276 260 265 270
279 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
280 275 280 285
283 Phe Val Gly Ala Tyr Thr Phe
284 290 295
287 <210> SEQ ID NO: 10
288 <211> LENGTH: 39
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Oligonucleotide c-myc 5'
295 <400> SEQUENCE: 10
296 gatccatgga gcagaagctg atctccgagg aggacctga

39

RAW SEQUENCE LISTING DATE: 06/04/2003
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Input Set : A:\ep.txt
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299 <210> SEQ ID NO: 11
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301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
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305 <223> OTHER INFORMATION: Oligonucleotide c-myc 3'
307 <400> SEQUENCE: 11
308 gatctcagg t ctcctcgga gatcagcttc tgctccatg 39
311 <210> SEQ ID NO: 12
312 <211> LENGTH: 45
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: 5' MCS oligonucleotide
319 <400> SEQUENCE: 12
320 gatctcggtc gacctgcattt caattcccggtt gtgcggccgc gagct 45
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324 <211> LENGTH: 37
325 <212> TYPE: DNA
326 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: 3' MCS oligonucleotide
331 <400> SEQUENCE: 13
332 cgcggccgca cccggaaattt gcatgcagg cgaccga 37
335 <210> SEQ ID NO: 14
336 <211> LENGTH: 22
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Oligonucleotide 3' mMBP1
343 <400> SEQUENCE: 14
344 cggtaactggc agaggtaact gg 22
347 <210> SEQ ID NO: 15
348 <211> LENGTH: 1513
349 <212> TYPE: DNA
350 <213> ORGANISM: Artificial Sequence
352 <220> FEATURE:
353 <223> OTHER INFORMATION: MBP1 murine (complete sequence)
355 <220> FEATURE:
356 <221> NAME/KEY: CDS
357 <222> LOCATION: (49)..(1377)
359 <400> SEQUENCE: 15
360 gctgtggcag aaaccctga cttctgccca ccacctccca gcctcagg atg ctc cct 57
361 Met Leu Pro
362 1
364 tt tttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg tt tttt ctg ctg 105
365 Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu
366 5 10 15
368 ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc 153
  
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/829,936B

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Input Set : A:\ep.txt

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